

Preparation for Term Paper (Genomic Heritability Calculations)

Review from [Barry et al. 2023](#) (*Figure 1*)

- **Family Based Designs**
 - Twin Studies
 - Extended Twin Design (including other relatives)
- **Genomic Methods: Unrelated Individuals**
 - Linkage Disequilibrium (*LD*) Score Regression
 - Supplemental Materials describe implementation in [LDSC](#) package ([Bulik-Sullivan et al. 2015](#)).
 - Genomic relatedness REstricted Maximum-Likelihood (***GREML***)
 - Part of [GCTA](#) (Genome-wide Complex Trait Analysis, [Yang et al. 2011](#))
 - [GCTA Wikipedia Entry](#)
 - LD- and MAF-stratified GREML (*GREML-LDMS*, [Yang et al. 2015](#))
- **Genomic Methods: Related Individuals**
 - *GREML-KIN* (GREML with KINship analysis – [Hill et al. 2018](#), [Xia et al. 2016](#), and/or [Zaitlen et al. 2013](#).
 - On the *GCTA* website, the section for “*GREML in family data*” references [Zaitlen et al. 2013](#).
 - ***Trio-GCTA*** ([Eilertsen et al. 2021](#))
 - Material (or Paternal) GCTA (*M-GCTA*, [Qiao et al. 2020](#))
 - Relatedness Disequilibrium Regression (***RDR***, [Young et al. 2018](#))
 - Supplemental Materials also reference [Visscher et al. 2006](#).
- *Table 1* also describes strengths and limitations, which include the relative estimated contribution of rare variants.
- *Box 1* defines narrow-sense heritability versus broad sense heritability.

Newer/Additional Methods

- *GPLEMMA* ([Kerin and Marchini 2020](#))
 - Cites **RDR** publication ([Young et al. 2018](#))
- *SAFE-h²* ([Darbani and Nicolaisen 2023](#))
 - Includes comparisons to *EMMAX* ([Kang et al. 2010](#)) and **LDAK**.
 - *EMMAX* = EMMA eXpedited, an extension of EMMA ([Kang et al. 2008](#)).
 - Two implementations for **LDAK** are mentioned. One is within *GCTA*, and the other is described as **LDAK-Thin** ([Speed et al. 2012](#)).
- The [GCTA webpage](#) lists *sBLUP* among available methods, but not necessarily for heritability?
 - *sBLUP* = Summary-level BLUP
 - Best Linear Unbiased Prediction ([BLUP](#)) is referenced in [Wang et al. 2019](#)
 - The *rrBLUP* (ridge-regression BLUP) R-package is a [dependency](#) for the *Bloom et al. 2019* code (imported in [mapping.R](#), for example).
- While not an additional method, [Tang et al. 2022](#) is an additional review on the general topic.
 - Includes descriptions of additional methods.
- [Srivastava et al. 2023](#) is another such review.
 - Describes [REML](#) (REstricted Maximum Likelihood, with applications in [Lee et al. 2006](#) and [Yang et al. 2010](#)) for individual-level data, before listing assumptions for **GREML** versus **LDAK**.
- *Bloom et al. 2019* references [de los Campos et al. 2015](#) (“*Genomic Heritability: What Is It?*”)
- [Evans et al. 2018](#) provides a comparison of different methods.
 - It looks like there is noticeable emphasis on implementation of *GREML* and *LDAK* methods.

Methods for Additional Focus

- Genomic relatedness REstricted Maximum-Likelihood (**GREML**)
 - Part of [GCTA](#) (Genome-wide Complex Trait Analysis, [Yang et al. 2011](#))
 - Can be cited as [Yang et al. 2010](#)
- Linkage-Disequilibrium Adjusted Kinships (**LDAK**, [Speed et al. 2012](#)).
- Relatedness Disequilibrium Regression (**RDR**, [Young et al. 2018](#))
- **Trio-GCTA** ([Eilertsen et al. 2021](#))
- “GREML-WGS” ([Wainschtein et al. 2022](#))
 - [Young 2019](#) used “GREML-WGS” to describe this method.
 - Plots in the publication describe using “GREML-LDMS”, but the data is Whole Genome Sequencing data (where I would expect that there should be no imputation).

Previous Related Discussions

- I have a *journal comment/question* for [Young 2019](#), which was referenced in the [Barry et al. 2023](#) review.
 - This was in turn referenced in a *preprint comment* for [Dolan et al. 2019](#), which specifically references **RDR** (in reference to *Young 2019* comment/question above) as well as **heritability**.
- I have *preprint comment* on an article titled “[Recovery of trait heritability from whole genome sequence data](#)” (with a later peer-reviewed version published in [Wainschtein et al. 2022](#)).
- As might be expected, “*heritability*” is mentioned in the [earlier preprint comment](#) for the *Bloom et al. 2019* data that I am (partially) [re-analyzing](#).
- Because data analysis was not performed, it may be somewhat off topic. However, there was mention to interpretation of heritability in a *preprint comment* on [Lowes et al. 2022](#).
- While not exactly about heritability, I have a *preprint comment* related to predicting height for [Thompson et al. 2022](#).
- Height is also briefly mentioned in a [Disqus](#) comment for [Marnetto et al. 2020](#), even if not currently visible on the journal website?.

Additional Reviews

(referenced by [Barry et al. 2023](#))

- In addition to the [Visscher et al. 2010](#) height GWAS article mentioned in the [Height QTL Notes](#), [Barry et al. 2023](#) reference a review related to heritability and genomics in [Visscher et al. 2008](#).
- A review by [Mayhew et al. 2017](#) is also referenced.
- [Yang et al. 2017](#) includes a figure related to estimation of height heritability with *different methods*.
- [Young 2019](#) includes a table showing variation in heritability values for height (with *different methods* and in different cohorts).
- [Zhu and Zhou 2020](#) is another cited review.